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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Soll, Dieter

(ii) TITLE OF INVENTION: GLU-TRAN AMIDOTRANSFERASE - A NOVEL
ESSENTIAL TRANSLATIONAL COMPONENT

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
- (B) STREET: 1800 M Street, N.W.
- (C) CITY: Washington
- (D) STATE: D.C.
- (E) COUNTRY: USA
- (F) ZIP: 20036-5869

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US Unassigned
- (B) FILING DATE: 03-FEB-1998
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/037,275
- (B) FILING DATE: 03-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Adler, Reid G.
- (B) REGISTRATION NUMBER: 30,988
- (C) REFERENCE/DOCKET NUMBER: 044574-5024-WO

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-467-7000
- (B) TELEFAX: 202-467-7176

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..54, 58..390, 394..1866, 1870..3303, 3310
.3321, 3325..3348, 3352..3429, 3433..3471, 3475
.3480, 3484..3495)

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xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAA TTC GAT CCT GTC TCA AGG IGT TTT GTT GCT TTA AAG GGC TTG TTT Glu Phe Asp Pro Val Ser Arg Arg Phe Val Ala Leu Lys Gly Leu Phe 1 5 10 15	45
. TTG ATA TGA TCA GTA TTA TAT GAC TTA ACG GAG AAA TAT GTG GAG GTG Leu Ile Ser Val Leu Tyr Asp Leu Thr Glu Lys Tyr Val Glu Val 20 25 30	96
. GAT CAT ATG TCA CGA ATT TCA ATA GAA GAA GTA AAG CAC GTT GCG CAC Asp His Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His 35 40 45	144
. CTT GCA AGA CTT GCG ATT ACT GAA GAA GCA AAA ATG TTC ACT GAA Leu Ala Arg Leu Ala Ile Thr Glu Glu Ala Lys Met Phe Thr Glu 50 55 60	192
. CAG CTC GAC AGT ATC ATT TCA TTT GCC GAG GAG CTT AAT GAG GTT AAC Gln Leu Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn 65 70 75	240
ACA GAC AAT GTG GAG CCT ACA ACT CAC GTG CTG AAA ATG AAA AAT GTC Thr Asp Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val 80 85 90 95	288
ATG AGA GAA GAT GAA GCG GGT AAA GGT CTT CCG GTT GAG GAT GTC ATG Met Arg Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met 100 105 110	336
AAA AAT GCG CCT GAC CAT AAA GAC GGC TAT ATT CGT GTG CCA TCA ATT Lys Asn Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile 115 120 125	384
CTG GAC TAA AGG AGG GAC ACA AGA ATG TCA TTA TTT GAT CAT AAA ATC Leu Asp Arg Arg Asp Thr Arg Met Ser Leu Phe Asp His Lys Ile 130 135 140	432
ACA GAA TTA AAA CAG CTC ATA CAT AAA AAA GAG ATT AAG ATT TCT GAT Thr Glu Leu Lys Gln Leu Ile His Lys Lys Glu Ile Lys Ile Ser Asp 145 150 155	480
CTG GTT GAT GAA TCT TAT AAA CGC ATC CAA GCG GTT GAT GAT AAG GTA Leu Val Asp Glu Ser Tyr Lys Arg Ile Gln Ala Val Asp Asp Lys Val 160 165 170	528
CAA GCC TTT TTG GCA TTA GAT GAA GAA AGA GCG CGC GCA TAC GCG AAG Gln Ala Phe Leu Ala Leu Asp Glu Glu Arg Ala Arg Ala Tyr Ala Lys 175 180 185 190	576
GAG CTT GAT GAG GCG GTT GAC GGC CGT TCT GAG CAC GGT CTT CTT TTC Glu Leu Asp Glu Ala Val Asp Gly Arg Ser Glu His Gly Leu Leu Phe 195 200 205	624
GGT ATG CCG ATC GGC GTA AAA GAT AAT ATC GTA ACA AAA GGG CTG CGC Gly Met Pro Ile Gly Val Lys Asp Asn Ile Val Thr Lys Gly Leu Arg 210 215 220	672

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ACA ACA TGC TCC AGC AAA ATT CTC GAA AAC TTT GAT CCG ATT TAC GAT Thr Thr Cys Ser Ser Lys Ile Leu Glu Asn Phe Asp Pro Ile Tyr Asp 225 230 235	701
GCT ACT GTC GTT CAG CGC CCT CAA GAC GCT GAA GCG GTC ACA ATC GGA Ala Thr Val Val Gln Arg Leu Gln Asp Ala Glu Ala Val Thr Ile Gly 240 245 250	762
AAA CTG AAC ATG GAC GAA TTC GCC ATG GGG TCA TCT ACA GAA AAC TCA Lys Leu Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser 255 260 265 270	816
GCT TAC AAG CTG ACG AAA AAC CCT TGG AAC CTG GAT ACA GTT CCC GGC Ala Tyr Lys Leu Thr Lys Asn Pro Trp Asn Leu Asp Thr Val Pro Gly 275 280 285	864
GGT TCA AGC GGC GGA TCT GCA GCT GCG GTT GCT GCG GGA GAA GTT CCG Gly Ser Ser Gly Ser Ala Ala Ala Val Ala Ala Gly Glu Val Pro 290 295 300	912
TTT TCT CTT GGA TCT GAC ACA GGC GGC TCC ATC CGT CAG CCG GCA TCT Phe Ser Leu Gly Ser Asp Thr Gly Ser Ile Arg Gln Pro Ala Ser 305 310 315	960
TTC TGC GGC GTT GTC GGA TTA AAA CCT ACA TAC GGA CGT GTA TCT CGT Phe Cys Gly Val Val Gly Leu Lys Pro Thr Tyr Gly Arg Val Ser Arg 320 325 330	1008
TAC GGC CTG GTC GCA TTT GCG TCT TCA TTG GAC CAA ATC GGA CCG ATT Tyr Gly Leu Val Ala Phe Ala Ser Ser Leu Asp Gln Ile Gly Pro Ile 335 340 345 350	1056
ACA CGT ACG GTT GAG GAT AAC GCG TTT TTA CTT CAA GCG ATT TCC GGC Thr Arg Thr Val Glu Asp Asn Ala Phe Leu Leu Gln Ala Ile Ser Gly 355 360 365	1104
GTA GAC AAA ATG GAC TCT ACG AGT GCA AAT GTG GAC GTG CCT GAT TTT Val Asp Lys Met Asp Ser Thr Ser Ala Asn Val Asp Val Pro Asp Phe 370 375 380	1152
CTT TCT TCA TTA ACT GGC GAC ATC AAA GGA CTG AAA ATC GCC GTT CCG Leu Ser Ser Leu Thr Gly Asp Ile Lys Gly Leu Lys Ile Ala Val Pro 385 390 395	1200
AAA GAA TAC CTT GGT GAA GGT GTC GGC AAA GAA GCG AGA GAA TCT GTC Lys Glu Tyr Leu Gly Glu Val Gly Lys Glu Ala Arg Glu Ser Val 400 405 410	1248
TTG GCA GCG CTG AAA GTC CTT GAA GGT CTC GGC GCT ACA TGG GAA GAA Leu Ala Ala Leu Lys Val Leu Glu Gly Leu Gly Ala Thr Trp Glu Glu 415 420 425 430	1296
GTG TCT CTT CCG CAC AGT AAA TAC GCG CTT GCG ACA TAT TAC CTG CTG Val Ser Leu Pro His Ser Lys Tyr Ala Leu Ala Thr Tyr Tyr Leu Leu 435 440 445	1344
TCA TCT TCT GAA GCG TCA GCG AAC CTT GCA CGC TTT GAC GGC ATC CGC Ser Ser Ser Glu Ala Ser Ala Asn Leu Ala Arg Phe Asp Gly Ile Arg 450 455 460	1392

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TAC GGC TAC CGC ACA GAC AAC GCG CAT AAC CTG ATC GAC CTT TAC AAG Tyr Gly Tyr Arg Thr Asp Asn Ala Asp Asn Leu Ile Asp Leu Tyr Lys 465 470 475	1441
CAA ACG CGC GCT GAA GGT TTC GGA ATT GAA GTC AAA CGC CGC ATC ATG Gln Thr Arg Ala Glu Gly Phe Gly Asn Glu Val Lys Arg Arg Ile Met 480 485 490	1489
CTC GGA ACG TTT GCT TTA AGC TCA GGC TAC TAC GAT GCG TAC TAC AAA Leu Gly Thr Phe Ala Leu Ser Ser Gly Tyr Tyr Asp Ala Tyr Tyr Lys 495 500 505 510	1536
AAA GCG CAA AAA GTG CGT ACG TTG ATT AAG AAG GAT TTC GAG GAC GTA Lys Ala Gln Lys Val Arg Thr Leu Ile Lys Lys Asp Phe Glu Asp Val 515 520 525	1584
TTT GAA AAA TAT GAT GTT ATT GTT GGA CCG ACT ACA CCG ACA CCT GCG Phe Glu Lys Tyr Asp Val Ile Val Gly Pro Thr Thr Pro Thr Pro Ala 530 535 540	1632
TTT AAA ATC GGT GAA AAC ACG AAG GAT CCG CTC ACA ATG TAC GCA AAC Phe Lys Ile Gly Glu Asn Thr Lys Asp Pro Leu Thr Met Tyr Ala Asn 545 550 555	1680
GAT ATC TTA ACG ATT CCG GTC AAC CTT GCG GCG TAC CCG GAA TCA GGT Asp Ile Leu Thr Ile Pro Val Asn Leu Ala Ala Tyr Arg Glu Ser Gly 560 565 570	1728
GCC ATG CGG TTA GCA GAC GGA CTT CCG CTC GGC CTG CAA ATC ATC GGA Ala Met Arg Leu Ala Asp Gly Leu Pro Leu Gly Leu Gln Ile Ile Gly 575 580 585 590	1776
AAA CAC TTT GAT GAA GCA CTG TAT ACC GCG TTG CTC ATG CAT TTG AAC Lys His Phe Asp Glu Ala Leu Tyr Thr Ala Leu Leu Met His Leu Asn 595 600 605	1824
AAG CAA CAG ACC ATC ATA AAG CAA AAC CTG AAC TGT AAG GGG Lys Gln Gln Thr Ile Ile Lys Gln Asn Leu Asn Cys Lys Gly 610 615 620	1866
TGA AAA GAA TTG AAC TTT GAA ACG GTA ATC GGA CTT GAA GTC CAC GTT Lys Glu Leu Asn Phe Glu Thr Val Ile Gly Leu Glu Val His Val 625 630 635	1914
GAG TTA AAA ACA AAA TCA AAA ATT TTC TCA AGC TCT CCA ACG CCA TTC Glu Leu Lys Thr Lys Ser Lys Ile Phe Ser Ser Pro Thr Pro Phe 640 645 650	1962
GGC GCG GAG GCG AAT ACG CAG ACA AGC GTT ATT GAC CTC GGA TAT CCG Gly Ala Glu Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro 655 660 665	2010
GGC GTC CTG CCT GTT CTG AAC AAA GAA GCC GTT GAA TTC GCA ATG AAA Gly Val Leu Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys 670 675 680	2058
GCC GCT ATG GCG CTC AAC TGT GAG ATC GCA ACG GAT ACG AAG TTT GAC Ala Ala Met Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp 685 690 695	2106

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CGC RAA AAC TAT TTC TAT CCT GAC AAC CCG AAA GCG TAT CAG ATT TCT Arg Lys Asn Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gin Ile Ser 700 705 710 715	3154
CAA TTT GAT AAG CCA ATC GGC CAA AAC GGC TGG ATC GAA ATT GAA GTC Gin Phe Asp Lys Pro Ile Gly Glu Asn Gly Trp Ile Glu Ile Gin Val 720 725 730	2202
GCG GGC AAA ACA AAA CGC ATC GGC ATC ACG CGC CTT CAT CTT GAA GAG Gly Gly Lys Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu 735 740 745	2250
GAT GCC GGA AAA CTG ACG CAT ACG GGC GAC GGC TAT TCT CTT GTT GAC Asp Ala Gly Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp 750 755 760	2298
TTC AAC CGT CAA GGA ACG CCG CTT GTT GAG TNC GTA TCA GAG CCG GAC Phe Asn Arg Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp 765 770 775	2346
ATC CGC ACG CCG GAA GAA NCG TAC GCA TAT CTT GAA AAG CTG AAA TCC Ile Arg Thr Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser 780 785 790 795	2394
ATC ATC CAA TAT ACA GGC GTT TCT GAC TGT AAA ATG GAA GAA GGC TCA Ile Ile Gin Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser 800 805 810	2442
CTT CGC TGT GAC GCC AAT ATC TCT CTT CGT CCG ATC GGC CAA GAG GAA Leu Arg Cys Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gin Glu Glu 815 820 825	2490
TTC GGC ACA AAA ACA GAA TTG AAA AAC TTG AAC TCC TTT GCG TTT GTT Phe Gly Thr Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val 830 835 840	2538
CAA AAA GGC CTT GAG CAT GAA GAA AAA CGC CAG GAG CAG GTT CTT CTT Gln Lys Gly Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu 845 850 855	2586
TCC GGC TTC TTC ATC CAG CAA GAA ACT CGC CGT TAT GAT GAA GCA ACG Ser Gly Phe Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr 860 865 870 875	2634
AAG AAA ACC ATT CTT ATG CGT GTC AAA GAG GGA TCT GAC GAC TAC CGT Lys Lys Thr Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg 880 885 890	2682
TAC TTC CCA GAG CCA GAT CTA GTC GAG CTC TAC ATT GAT GAT GAA TGG Tyr Phe Pro Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp 895 900 905	2730
AAG GAA CGC GTA AAA GCA AGC ATT CCT GAG CTT CCG GAT GAG CGC CGC Lys Glu Arg Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg 910 915 920	2778
AAG CGT TAT ATC GAA GAG CTT GGC TTC GCT GCA TAT GAC GCA ATG GTT Lys Arg Tyr Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val 925 930 935	2826

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CTG ACG CTG ACA AAA GAA ATG GCT GAT TTC TTC GAA GAA ACC GTT CAA Ieu Thr Ieu Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Glu 940 945 950 955	2974
AAA GGC GCT GAA GCT AAA CAA GCG TCT AAC TGG CTG ATG GGT GAA GTG Lys Gly Ala Glu Ala Lys Glu Ala Ser Asn Trp Leu Met Gly Glu Val 960 965 970	2982
TCA GCT TAC CTA AAC GCA GAA CAA AAA GAG CTT GCC GAT GTT GCC CTG Ser Ala Tyr Leu Asn Ala Glu Glu Leu Ala Asp Val Ala Leu 975 980 985	2970
ACA CCT GAA GGC CTT GCC GGC ATG ATC AAA TTG ATT GAA AAA GGA ACC Thr Pro Glu Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr 990 995 1000	3018
ATT TCT TCT AAG ATC GCG AAG AAA GTG TTT AAA GAA TTG ATT GAA AAA Ile Ser Ser Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys 1005 1010 1015	3066
GCC GGC GAC GCT GAG AAG ATT GTG AAA GAG AAA GGC CTT GTT CAG ATT Gly Gly Asp Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile 1020 1025 1030 1035	3114
TCT GAC GAA GGC GTG CTT CTG AAG CTT GTC ACT GAG GCG CTT GAC AAC Ser Asp Glu Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn 1040 1045 1050	3162
AAT CCT CAA TCA ATC GAA GAC TTT AAA AAC GGA AAA GAC CGC GCG ATC Asn Pro Gln Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile 1055 1060 1065	3210
GCC TTC CTA GTC GGA CAG ATT ATG AAA GCG TCC AAA GGA CAA GCC AAC Gly Phe Leu Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn 1070 1075 1080	3258
CCG CCG ATG GTC AAC AAA ATT CTG CTT GAA GAA ATT AAA AAA CGC Pro Pro Met Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg 1085 1090 1095	3303
TAATAA AAA AGC AGC CCT TAG AGG CTG CTT TTT TTA TGG TCA AAT Lys Ser Ser Pro Arg Leu Leu Phe Leu Trp Ser Asn 1100 1105 1110	3348
TGA GAT AAA GAC AAG ATG AGG GCC CGA AGC CTT TCA ACT TCT TTG TCG Asp Lys Asp Lys Met Arg Ala Arg Ser Leu Ser Thr Ser Leu Ser 1115 1120 1125	3396
TTG GTT CCG GCC AAA TTG GAC AGC ATG CCT TTA TAA TCG GCT TGC GCG Leu Val Pro Ala Lys Leu Asp Ser Met Pro Leu Ser Ala Cys Ala 1130 1135 1140	3444
GTT TAT CCT GAG TCA ATT CTT CCT CGA TAA GAT AAG TGA CAC GGT GAT Val Tyr Pro Glu Ser Ile Leu Pro Arg Asp Lys His Gly Asp 1145 1150	3492
ATC Ile 1155	3495

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2: INFORMATION FOR SEQ ID NO:2:

11) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Phe Asp Pro Val Ser Arg Arg Phe Val Ala Leu Lys Gly Leu Phe
1 5 10 15

Leu Ile Ser Val Leu Tyr Asp Leu Thr Glu Lys Tyr Val Glu Val Asp
20 25 30

His Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu
35 40 45

Ala Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln
50 55 60

Leu Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr
65 70 75 80

Asp Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met
85 90 95

Arg Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys
100 105 110

Asn Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu
115 120 125

Asp Arg Arg Asp Thr Arg Met Ser Leu Phe Asp His Lys Ile Thr Glu
130 135 140

Leu Lys Gln Leu Ile His Lys Lys Glu Ile Lys Ile Ser Asp Leu Val
145 150 155 160

Asp Glu Ser Tyr Lys Arg Ile Gln Ala Val Asp Asp Lys Val Gln Ala
165 170 175

Phe Leu Ala Leu Asp Glu Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu
180 185 190

Asp Glu Ala Val Asp Gly Arg Ser Glu His Gly Leu Leu Phe Gly Met
195 200 205

Pro Ile Gly Val Lys Asp Asn Ile Val Thr Lys Gly Leu Arg Thr Thr
210 215 220

Cys Ser Ser Lys Ile Leu Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr
 225 230 235 240

Val Val Gln Arg Leu Gln Asp Ala Glu Ala Val Thr Ile Gly Lys Leu
245 250 255

Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr
160 165 170

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Lys Ieu Thr Lys Asn Pro Trp Asn Leu Asp Thr Val Pro Gly Gly Ser
 275 280 285
 Ser Gly Gly Ser Ala Ala Ala Val Ala Ala Gly Glu Val Pro Phe Ser
 290 295 300
 Leu Gly Ser Asp Thr Gly Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys
 305 310 315 320
 Gly Val Val Gly Leu Lys Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly
 325 330 335
 Leu Val Ala Phe Ala Ser Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg
 340 345 350
 Thr Val Glu Asp Asn Ala Phe Leu Leu Gln Ala Ile Ser Gly Val Asp
 355 360 365
 Lys Met Asp Ser Thr Ser Ala Asn Val Asp Val Pro Asp Phe Leu Ser
 370 375 380
 Ser Leu Thr Gly Asp Ile Lys Gly Leu Lys Ile Ala Val Pro Lys Glu
 385 390 395 400
 Tyr Leu Gly Glu Gly Val Gly Lys Glu Ala Arg Glu Ser Val Leu Ala
 405 410 415
 Ala Leu Lys Val Leu Glu Gly Leu Gly Ala Thr Trp Glu Glu Val Ser
 420 425 430
 Leu Pro His Ser Lys Tyr Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser
 435 440 445
 Ser Glu Ala Ser Ala Asn Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly
 450 455 460
 Tyr Arg Thr Asp Asn Ala Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr
 465 470 475 480
 Arg Ala Glu Gly Phe Gly Asn Glu Val Lys Arg Arg Ile Met Leu Gly
 485 490 495
 Thr Phe Ala Leu Ser Ser Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala
 500 505 510
 Gln Lys Val Arg Thr Leu Ile Lys Lys Asp Phe Glu Asp Val Phe Glu
 515 520 525
 Lys Tyr Asp Val Ile Val Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys
 530 535 540
 Ile Gly Glu Asn Thr Lys Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile
 545 550 555 560
 Leu Thr Ile Pro Val Asn Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met
 565 570 575
 Arg Leu Ala Asp Gly Leu Pro Leu Gly Leu Gln Ile Ile Gly Lys His
 580 585 590

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Phe Asp Glu Ala Leu Tyr Thr Ala Leu Leu Met His Leu Asn Lys Gin
 595 600 605

Gin Thr Ile Ile Lys Gln Asn Leu Asn Cys Lys Gly Lys Glu Leu Asn
 610 615 620

Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys Thr Lys
 625 630 635 640

Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu Ala Asn
 645 650 655

Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu Pro Val
 660 665 670

Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met Ala Leu
 675 680 685

Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn Tyr Phe
 690 695 700

Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp Lys Pro
 705 710 715 720

Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys Thr Lys
 725 730 735

Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly Lys Leu
 740 745 750

Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg Gln Gly
 755 760 765

Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr Pro Glu
 770 775 780

Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln Tyr Thr
 785 790 795 800

Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys Asp Ala
 805 810 815

Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Lys Thr
 820 825 830

Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly Leu Glu
 835 840 845

His Glu Glu Lys Arg Gln Gln Val Leu Leu Ser Gly Phe Phe Ile
 850 855 860

Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr Ile Leu
 865 870 875 880

Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro Glu Pro
 885 890 895

Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg Val Lys
 900 905 910

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Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr Ile Gln
925          920          925

Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu Thr Lys
930          935          940

Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala Glu Ala
945          950          955          960

Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr Leu Asn
965          970          975

Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu Gly Leu
980          985          990

Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser Lys Ile
995          1000         1005

Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp Ala Glu
1010         1015         1020

Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu Gly Val
1025         1030         1035         1040

Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln Ser Ile
1045         1050         1055

Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu Val Gly
1060         1065         1070

Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met Val Asn
1075         1080         1085

Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg Lys Ser Ser Pro Arg Leu
1090         1095         1100

Leu Phe Leu Trp Ser Asn Asp Lys Asp Lys Met Arg Ala Arg Ser Leu
1105         1110         1115         1120

Ser Thr Ser Leu Ser Leu Val Pro Ala Lys Leu Asp Ser Met Pro Leu
1125         1130         1135

Ser Ala Cys Ala Val Tyr Pro Glu Ser Ile Leu Pro Arg Asp Lys His
1140         1145         1150

Gly Asp Ile
1155

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

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'51 LOCATION: 1..1458

'xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCA TTA TTT GAT CAT AAA ATC ACA GAA TCA AAA CAG CTC ATA CAT Met Ser Leu Phe Asp His Lys Ile Thr Glu Leu Lys Gln Leu Ile His 1 5 10 15	45
AAA AAA GAG ATT AAG ATT TCT GAT CTG GTT GAT GAA TCT TAT AAA CGC Lys Lys Glu Ile Lys Ile Ser Asp Leu Val Asp Glu Ser Tyr Lys Arg 10 25 30	96
ATC CAA GCG GTT GAT GAT AAG GTA CAA GCC TTT TTG GCA TTA GAT GAA Ile Gln Ala Val Asp Asp Lys Val Gln Ala Phe Leu Ala Leu Asp Glu 35 40 45	144
GAA AGA GCG CGC GCA TAC GCG AAG GAG CTT GAT GAG GCG GTT GAC GGC Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly 50 55 60	192
CGT TCT GAG CAC GGT CTT CTT TTC GGT ATG CCG ATC GGC GTA AAA GAT Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp 65 70 75 80	240
AAT ATC GTA ACA AAA GGG CTG CGC ACA ACA TGC TCC AGC AAA ATT CTC Asn Ile Val Thr Lys Gly Leu Arg Thr Thr Cys Ser Ser Lys Ile Leu 85 90 95	288
GAA AAC TTT GAT CCG ATT TAC GAT GCT ACT GTC GTT CAG CGC CTT CAA Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr Val Val Gln Arg Leu Gln 100 105 110	336
GAC GCT GAA GCG GTC ACA ATC GGA AAA CTG AAC ATG GAC GAA TTC GCC Asp Ala Glu Ala Val Thr Ile Gly Lys Leu Asn Met Asp Glu Phe Ala 115 120 125	384
ATG GGG TCA TCT ACA GAA AAC TCA GCT TAC AAG CTG ACG AAA AAC CCT Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr Lys Leu Thr Lys Asn Pro 130 135 140	432
TGG AAC CTG GAT ACA GTT CCC GGC GGT TCA AGC GGC GGA TCT GCA GCT Trp Asn Leu Asp Thr Val Pro Gly Ser Ser Gly Gly Ser Ala Ala 145 150 155 160	480
GCG GTT GCT GCG GGA GAA GTT CCG TTT TCT CTT GGA TCT GAC ACA GGC Ala Val Ala Ala Gly Glu Val Pro Phe Ser Leu Gly Ser Asp Thr Gly 165 170 175	528
GGC TCC ATC CGT CAG CCG GCA TCT TTC TGC GGC GTT GTC GGA TTA AAA Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys Gly Val Val Gly Leu Lys 180 185 190	576
CCT ACA TAC GGA CGT GTA TCT CGT TAC GGC CTG GTC GCA TTT GCG TCT Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly Leu Val Ala Phe Ala Ser 195 200 205	624
TCA TTG GAC CAA ATC GGA CCG ATT ACA CGT ACG GTT GAG GAT AAC GCG Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg Thr Val Glu Asp Asn Ala 210 215 220	672

TTT TTA CTT CAA GCG ATT TCC GGC GTA GAC AAA ATG GAC TCT ACG AGT Phe Leu Leu Gln Ala Ile Ser Gly Val Asp Lys Met Asp Ser Thr Ser 225 230 235 240	721
GCA AAT GTG GAC GTG CCT GAT TTT CTT TCT TCA TTA ACT GGC GAC ATC Ala Asn Val Asp Val Pro Asp Phe Leu Ser Ser Leu Thr Gly Asp Ile 245 250 255	769
AAA GGA CTG AAA ATC GCC GTT CCG AAA GAA TAC CTT GGT GAA GGT GTC Lys Gly Leu Lys Ile Ala Val Pro Lys Glu Tyr Leu Gly Glu Gly Val 260 265 270	816
GGC AAA GAA GCG AGA GAA TCT GTC TTG GCA GCG CTG AAA GTC CTT GAA Gly Lys Glu Ala Arg Glu Ser Val Leu Ala Ala Leu Lys Val Leu Glu 275 280 285	864
GGT CTC GGC GCT ACA TGG GAA GAA GTG TCT CTT CCG CAC AGT AAA TAC Gly Leu Gly Ala Thr Trp Glu Glu Val Ser Leu Pro His Ser Lys Tyr 290 295 300	912
GCG CTT GCG ACA TAT TAC CTG CTG TCA TCT TCT GAA GCG TCA GCG AAC Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser Glu Ala Ser Ala Asn 305 310 315 320	960
CTT GCA CGC TTT GAC GGC ATC CGC TAC GGC TAC CGC ACA GAC AAC GCG Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Thr Asp Asn Ala 325 330 335	1008
GAT AAC CTG ATC GAC CTT TAC AAG CAA ACG CGC GCT GAA GGT TTC GGA Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr Arg Ala Glu Gly Phe Gly 340 345 350	1056
AAT GAA GTC AAA CGC CGC ATC ATG CTC GGA ACG TTT GCT TTA AGC TCA Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser 355 360 365	1104
GGC TAC TAC GAT GCG TAC TAC AAA AAA GCG CAA AAA GTG CGT ACG TTG Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala Gln Lys Val Arg Thr Leu 370 375 380	1152
ATT AAG AAG GAT TTC GAG GAC GTA TTT GAA AAA TAT GAT GTT ATT GTT Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val 385 390 395 400	1200
GGA CCG ACT ACA CCG ACA CCT GCG TTT AAA ATC GGT GAA AAC ACG AAG Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys 405 410 415	1248
GAT CCG CTC ACA ATG TAC GCA AAC GAT ATC TTA ACG ATT CCG GTC AAC Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn 420 425 430	1296
CTT GCG GCG TAC CGG GAA TCA GGT GCC ATG CGG TTA GCA GAC GGA CTT Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu 435 440 445	1344
CCG CTC GGC CTG CAA ATC ATC GGA AAA CAC TTT GAT GAA GCA CTG TAT Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr 450 455 460	1392

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ACC GCG TTG CTG ATG CAT TTG AAC AAG CAA CAG ACC ATC ATA AAG CAA
 Thr Ala Leu Leu Met His Leu Asn Lys Gln Gln Thr Ile Ile Lys Gln
 +65 470 475 480

AAC CTG AAC TGT AAG GGG TGA
 Asn Leu Asn Cys Lys Gly
 485

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Leu	Phe	Asp	His	Lys	Ile	Thr	Glu	Leu	Lys	Gln	Leu	Ile	His
1					5				10				15		
Lys	Lys	Glu	Ile	Lys	Ile	Ser	Asp	Leu	Val	Asp	Glu	Ser	Tyr	Lys	Arg
			20					25				30			
Ile	Gln	Ala	Val	Asp	Asp	Lys	Val	Gln	Ala	Phe	Leu	Ala	Leu	Asp	Glu
			35				40				45				
Glu	Arg	Ala	Arg	Ala	Tyr	Ala	Lys	Glu	Leu	Asp	Glu	Ala	Val	Asp	Gly
			50				55			60					
Arg	Ser	Glu	His	Gly	Leu	Leu	Phe	Gly	Met	Pro	Ile	Gly	Val	Lys	Asp
			65				70		75			80			
Asn	Ile	Val	Thr	Lys	Gly	Leu	Arg	Thr	Thr	Cys	Ser	Ser	Lys	Ile	Leu
			85					90				95			
Glu	Asn	Phe	Asp	Pro	Ile	Tyr	Asp	Ala	Thr	Val	Val	Gln	Arg	Leu	Gln
			100				105			110					
Asp	Ala	Glu	Ala	Val	Thr	Ile	Gly	Lys	Leu	Asn	Met	Asp	Glu	Phe	Ala
			115				120			125					
Met	Gly	Ser	Ser	Thr	Glu	Asn	Ser	Ala	Tyr	Lys	Leu	Thr	Lys	Asn	Pro
			130				135			140					
Trp	Asn	Leu	Asp	Thr	Val	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ala	Ala
			145				150		155				160		
Ala	Val	Ala	Ala	Gly	Glu	Val	Pro	Phe	Ser	Leu	Gly	Ser	Asp	Thr	Gly
			165				170				175				
Gly	Ser	Ile	Arg	Gln	Pro	Ala	Ser	Phe	Cys	Gly	Val	Val	Gly	Leu	Lys
			180				185			190					
Pro	Thr	Tyr	Gly	Arg	Val	Ser	Arg	Tyr	Gly	Leu	Val	Ala	Phe	Ala	Ser
			195				200			205					
Ser	Leu	Asp	Gln	Ile	Gly	Pro	Ile	Thr	Arg	Thr	Val	Glu	Asp	Asn	Ala
			210				215			220					

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Phe Leu Leu Gln Ala Ile Ser Gly Val Asp Lys Met Asp Ser Thr Ser
 225 230 235 240

Ala Asn Val Asp Val Pro Asp Phe Leu Ser Ser Leu Thr Gly Asp Ile
 245 250 255

Lys Gly Leu Lys Ile Ala Val Pro Lys Glu Tyr Leu Gly Glu Gly Val
 260 265 270

Gly Lys Glu Ala Arg Glu Ser Val Leu Ala Ala Leu Lys Val Leu Glu
 275 280 295

Gly Leu Gly Ala Thr Trp Glu Glu Val Ser Leu Pro His Ser Lys Tyr
 290 295 300

Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser Glu Ala Ser Ala Asn
 305 310 315 320

Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Thr Asp Asn Ala
 325 330 335

Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr Arg Ala Glu Gly Phe Gly
 340 345 350

Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser
 355 360 365

Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala Gln Lys Val Arg Thr Leu
 370 375 380

Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val
 385 390 395 400

Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys
 405 410 415

Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn
 420 425 430

Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu
 435 440 445

Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr
 450 455 460

Thr Ala Leu Leu Met His Leu Asn Lys Gln Gln Thr Ile Ile Lys Gln
 465 470 475 480

Asn Leu Asn Cys Lys Gly
 485

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

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IX) FEATURE:

- (A) NAME/KEY: CCS
- (B) LOCATION: 1..1426

'xi' SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTC AAC TTT GAA ACG CTA ATC GGA CTT GAA GTC SAC GTT GAG TTA AAA Leu Asn Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys 1 5 10 15	49
ACA AAA TCA AAA ATT TTC TCA AGC TCT CCA ACG CCA TTC GGC GCG GAG Thr Lys Ser Lys Ile Phe Ser Ser Pro Thr Pro Phe Gly Ala Glu 20 25 30	96
GCG AAT ACG CAG ACA AGC GTT ATT GAC CTC GGA TAT CCG GGC GTC CTG Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu 35 40 45	144
CCT GTT CTG AAC AAA GAA GCC GTT GAA TTC GCA ATG AAA GCC GCT ATG Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met 50 55 60	192
GCG CTC AAC TGT CAC ATC GCA ACG GAT ACG AAG TTT GAC CGC AAA AAC Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn 65 70 75 80	240
TAT TTC TAT CCT GAC AAC CCG AAA GCG TAT CAG ATT TCT CAA TTT GAT Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp 85 90 95	288
AAG CCA ATC GGC GAA AAC GGC TGG ATC GAA ATT GAA GTC GGC GGC AAA Lys Pro Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys 100 105 110	336
ACA AAA CGC ATC GGC ATC ACG CGC CTT CAT CTT GAA GAG GAT GCC GGA Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Asp Ala Gly 115 120 125	384
AAA CTG ACG CAT ACG GGC GAC GGC TAT TCT CTT GTC AAC CGT Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg 130 135 140	432
CAA GGA ACG CCG CTT GTT GAG TNC GTA TCA GAG CCG GAC ATC CGC ACG Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr 145 150 155 160	480
CCG GAA GAA NCG TAC GCA TAT CTT GAA AAG CTG AAA TCC ATC ATC CAA Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln 165 170 175	528
TAT ACA GGC GTT TCT GAC TGT AAA ATG GAA GAA GGC TCA CTT CGC TGT Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys 180 185 190	576
SAC GCC AAT ATC TCT CTT CGT CCG ATC GGC CAA GAG GAA TTC GGC ACA Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr 195 200 205	624

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AAA ACA GAA TTG AAA AAC TTG AAC TCC TTT GCG TTT GTT CAA AAA GGC Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gin Cys Gly 210 215 220	6^1
CTT GAG CAT GAA GAA AAA CGC CAG GAG CAG GGT CTT CTT TCC GGC TTC Leu Glu His Glu Glu Lys Arg Gln Glu Gin Val Ile Leu Ser Gly Phe 225 230 235 240	722
TTC ATC CAG CAA GAA ACT CGC CGT TAT GAT GAA GCA ACG AAG AAA ACC Phe Ile Glu Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Thr Lys Thr 245 250 255	762
ATT CTT ATG CGT GTC AAA GAG GGA TCT GAC GAC TAC CGT TAC TTC CCA Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro 260 265 270	816
GAG CCA GAT CTA GTC GAG CTC TAC ATT GAT GAT GAA TGG AAG GAA CGC Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg 275 280 285	864
GTA AAA GCA AGC ATT CCT GAG CTT CCG GAT GAG CGC CGC AAG CGT TAT Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr 290 295 300	912
ATC GAA GAG CTT GGC TTC GCT GCA TAT GAC GCA ATG GTT CTG ACG CTG Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu 305 310 315 320	960
ACA AAA GAA ATG GCT GAT TTC TTC GAA GAA ACC GTT CAA AAA GGC GCT Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala 325 330 335	1008
GAA GCT AAA CAA GCG TCT AAC TGG CTG ATG GGT GAA GTG TCA GCT TAC Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr 340 345 350	1056
CTA AAC GCA GAA CAA AAA GAG CTT GCC GAT GTT GCC CTG ACA CCT GAA Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu 355 360 365	1104
GGC CTT GCC GGC ATG ATC AAA TTG ATT GAA AAA GGA ACC ATT TCT TCT Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser 370 375 380	1152
AAG ATC GCG AAG AAA GTG TTT AAA GAA TTG ATT GAA AAA GGC GGC GAC Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp 385 390 395 400	1200
GCT GAG AAG ATT GTG AAA GAG AAA GGC CTT GTT CAG ATT TCT GAC GAA Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu 405 410 415	1248
GGC GTG CTT CTG AAG CTT GTC ACT GAG GCG CTT GAC AAC AAT CCT CAA Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln 420 425 430	1296
TCA ATC GAA GAC TTT AAA AAC GGA AAA GAC CGC GCG ATC GGC TTC CTA Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu 435 440 445	1344

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GTC GGA CAG ATT ATG AAA GCG TCC AAA GGA CAA GCC AAC CCG CCG ATG
 Val Gly Gin Ile Met Lys Ala Ser Lys Gly Gin Ala Asn Pro Pro Met
 450 455 460

GTC AAC AAA ATT CTG CTT GAA GAA ATT AAA AAA CGC TAA
 Val Asn Lys Ile Leu Leu Gin Glu Ile Lys Lys Arg
 465 470 475

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Asn Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys
 1 5 10 15

Thr Lys Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu
 20 25 30

Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu
 35 40 45

Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met
 50 55 60

Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn
 65 70 75 80

Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp
 85 90 95

Lys Pro Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys
 100 105 110

Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly
 115 120 125

Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg
 130 135 140

Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr
 145 150 155 160

Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln
 165 170 175

Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys
 180 185 190

Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr
 195 200 205

Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly
 210 215 220

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Leu Glu His Glu Glu Lys Arg Gln Glu Glu Val Ile Ile Ser Gly Phe
 225 230 235 240
 Phe Ile Gin Gin Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr
 245 250 255
 Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro
 260 265 270
 Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg
 275 280 285
 Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr
 290 295 300
 Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu
 305 310 315 320
 Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala
 325 330 335
 Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr
 340 345 350
 Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu
 355 360 365
 Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser
 370 375 380
 Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp
 385 390 395 400
 Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu
 405 410 415
 Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln
 420 425 430
 Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu
 435 440 445
 Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met
 450 455 460
 Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg
 465 470 475

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:

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A) NAME/KEY: CDS
B) LOCATION: 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCA CGA ATT TCA ATA GAA GAA GTC AAG CAC GTT GCG CAC CTT GCA Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu Ala	48
1 5 10 15	
 AGA CCT GCG ATT ACT GAA GAA GAA GCA AAA ATG TTC ACT GAA CAG CTC Arg Leu Ala Ile Thr Glu Glu Ala Lys Met Phe Thr Glu Gin Leu	96
20 25 30	
 GAC AGT ATC ATT TCA TTT CCC GAG GAG CTT AAT GAG GTT AAC ACA GAC Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp	144
35 40 45	
 AAT GTG GAG CCT ACA ACT CAC GTG CTG AAA ATG AAA AAT GTC ATG AGA Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg	192
50 55 60	
 GAA GAT GAA GCG GGT AAA GGT CTT CCG GTT GAG GAT GTC ATG AAA AAT Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn	240
65 70 75 80	
 GCG CCT GAC CAT AAA GAC GGC TAT ATT CGT GTG CCA TCA ATT CTG GAC Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp	288
85 90 95	
 TAA	291

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: